GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:23:59 ; Search time 525 Seconds
(without alignments)
5007.645 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/1_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/H_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
7: /cgn2_6/ptodata/1/ina/PP_COMB.seq:*
8: /cgn2_6/ptodata/1/ina/RE_COMB.seq:*
9: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1250.4	84.5	1471	3	US-10-085-871C-2	Sequence 2, Appli
2	1235.2	83.5	1480	3	US-09-622-201-1	Sequence 1, Appli
3	1235.2	83.5	1480	3	US-09-622-201-2	Sequence 2, Appli
4	1228.4	83.1	1437	3	US-10-085-871C-1	Sequence 1, Appli
5	1166.8	78.9	4403765	3	US-09-103-840A-2	Sequence 2, Appli
6	1166.8	78.9	4411529	3	US-09-103-840A-1	Sequence 1, Appli
7	1135.8	76.8	1464	2	US-08-938-858-1	Sequence 1, Appli
8	1135.8	76.8	1464	3	US-09-726-774-7	Sequence 7, Appli
9	1118.6	75.6	1475	3	US-08-641-291A-92	Sequence 92, Appl
c 10	1109	75.0	36241	3	US-08-311-731A-134	Sequence 134, App
c 11	1109	75.0	36470	3	US-08-311-731A-123	Sequence 123, App
12	1096.6	74.1	1422	3	US-09-252-806-10	Sequence 10, Appl
13	1096.6	74.1	1422	3	US-09-711-508-10	Sequence 10, Appl
c 14	1095	74.0	1449	3	US-09-735-567-5	Sequence 5, Appli
15	1092	73.8	1460	3	US-09-463-618A-1	Sequence 1, Appli
16	1092	73.8	1460	3	US-10-062-777-1	Sequence 1, Appli
17	1076.2	72.8	1388	3	US-09-504-358-49	Sequence 49, Appl
18	1076.2	72.8	1388	3	US-09-954-314-49	Sequence 49, Appl
19	1076.2	72.8	1388	3	US-10-230-562-49	Sequence 49, Appl
20	981.8	66.4	1584	3	US-09-949-230A-1	Sequence 1, Appli
21	937.2	63.4	1477	3	US-09-606-401B-1	Sequence 1, Appli
22	891.8	60.3	1517	3	US-09-248-528-2	Sequence 2, Appli
23	891.8	60.3	1517	3	US-09-549-108-2	Sequence 2, Appli
24	891.8	60.3	1517	3	US-09-549-111-2	Sequence 2, Appli
25	891.8	60.3	1517	3	US-09-549-106-2	Sequence 2, Appli
26	891.8	60.3	1517	3	US-09-550-394-2	Sequence 2, Appli
27	889.2	60.1	1516	3	US-09-248-528-3	Sequence 3, Appli
28	889.2	60.1	1516	3	US-09-549-108-3	Sequence 3, Appli
29	889.2	60.1	1516	3	US-09-549-111-3	Sequence 3, Appli
30	889.2	60.1	1516	3	US-09-549-106-3	Sequence 3, Appli
31	889.2	60.1	1516	3	US-09-550-394-3	Sequence 3, Appli
32	889.2	60.1	1516	3	US-09-426-868-1	Sequence 1, Appli
33	885.2	59.9	1529	3	US-09-938-035B-1	Sequence 1, Appli
34	883.4	59.7	1529	3	US-09-938-035B-2	Sequence 2, Appli
35	882.8	59.7	1547	3	US-10-296-129-1	Sequence 1, Appli
36	877.4	59.3	1512	3	US-08-995-960-2	Sequence 2, Appli
37	876.4	59.3	1567	3	US-09-375-932A-4	Sequence 4, Appli
38	876.4	59.3	1567	3	US-10-156-562A-4	Sequence 4, Appli
39	871.6	58.9	1540	3	US-09-228-184-1	Sequence 1, Appli
40	871.6	58.9	1540	3	US-09-967-376-1	Sequence 1, Appli
c 41	869	58.8	3169	3	US-09-710-279-3356	Sequence 3356, Ap
42	869	58.8	3308	3	US-09-710-279-3905	Sequence 3905, Ap
43	868.2	58.7	1555	2	US-08-757-653-160	Sequence 160, App
44	868.2	58.7	1555	3	US-08-520-946-160	Sequence 160, App
45	868.2	58.7	1555	3	US-09-655-378A-160	Sequence 160, App

ALIGNMENTS

RESULT 1
US-10-085-871C-2
; Sequence 2, Application US/10085871C
; Patent No. 6716615
; GENERAL INFORMATION:
; APPLICANT: Lee, Fang-Yu
; APPLICANT: Lee, Ming-Liang
; APPLICANT: Anderson, Hong C.
; APPLICANT: Chiu, Schung-Ching
; TITLE OF INVENTION: New Strains of Saccharaothrix, Process for Producing Pravastain
; TITLE OF INVENTION: Strains and Isolation Process of (HMG)-COA Reductase
; FILE REFERENCE: 004135.P005
; CURRENT APPLICATION NUMBER: US/10/085,871C
; CURRENT FILING DATE: 2002-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Saccharothrix 45494
US-10-085-871C-2

Query Match 84.5%; Score 1250.4; DB 3; Length 1471;
Best Local Similarity 91.9%; Pred. No. 0;
Matches 1342; Conservative 0; Mismatches 116; Indels 2; Gaps 2;

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Qy          21 GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGGAAAGGCCCTTCGGGGTAC 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db           1 GACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGCGGTAAGGCCCTTCGGGGTAC 60

Qy          81 TCGAGCGGCGAACGGGTGAGTAACACGTGAGTAACCTGCCCCAGGCTTTGGGATAACCCC 140
               |||||||||||||||||||||||||||||| ||||||||||    ||  ||||||| ||
Db          61 ACGAGCGGCGAACGGGTGAGTAACACGTGGGTAACCTGCCCTGTACTCCGGGATAAGCCT 120

Qy         141 GGGAAACCGGGGCTAATACCGGATATGACCATCTGTCGCATGGTGGGTGGTGGAAAGATT 200
               |||||||  || |||||||||||||| ||||    |  ||||  || | ||||||||| |
Db         121 GGGAAACTAGGTCTAATACCGGATACGACCCCATAAGGCATCTTGTGGGGTGGAAAGTTC 180

Qy         201 TTTTGGCTTGGGATGGGCTCGCGGCCTATCAGCTTGTTGGTGGGGTGATGGCCTACCAAG 260
               ||  |||||||| | ||||||||||||||||||||||||||||||||||||||||||||
Db         181 CGGCGGTATGGGATGGACCCGCGGCCTATCAGCTTGTTGGTGGGGTGATGGCCTACCAAG 240

Qy         261 GCGGCGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGACTGAGACACGGCCC 320
               ||| ||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db         241 GCGACGACGGGTAGCCGGCCTGAGAGGGTGACCGGCCACACTGGGACTGAGACACGGCCC 300

Qy         321 AGACTCCTACGGGAGGCAGCAGTGGGGAATCTTGCACAATGGGCGGAAGCCTGATGCAGC 380
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GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:15:50 ; Search time 6468 Seconds
(without alignments)
10698.530 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: gb_est3:*
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7: gb_est6:*
8: gb_est7:*
9: gb_gss1:*
10: gb_gss2:*
11: gb_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	817	55.2	6499	9	BH771024	BH771024 LLMGtag74
	2	753.6	51.0	1954	8	CX109203	CX109203 RECm0593
	3	752.2	50.9	874	7	CO365133	CO365133 RTK1_23_G
c	4	705.2	47.7	887	10	CL693661	CL693661 PRI0162a_
c	5	607.6	41.1	1053	9	BZ447500	BZ447500 BONKF40TR
	6	606.8	41.0	1084	9	BZ439740	BZ439740 BONDU54TF
	7	594.8	40.2	1077	9	BZ450751	BZ450751 BONBQ63TR
c	8	594.6	40.2	744	9	BZ781734	BZ781734 ii31b08.g
	9	593	40.1	1079	9	BH705272	BH705272 BOMKA47TF
c	10	592.6	40.1	1031	9	BH656222	BH656222 BOMJZ86TF
c	11	587.6	39.7	1010	9	BZ431523	BZ431523 BONHD88TF
c	12	583.4	39.4	1016	9	BZ426201	BZ426201 BONDZ28TF
c	13	577.2	39.0	1044	9	BZ463550	BZ463550 BONKC86TF
c	14	573.4	38.8	1051	9	BZ494182	BZ494182 BONHR54TR
c	15	571.6	38.6	1054	9	BH647750	BH647750 BOMND31TR
c	16	557.4	37.7	663	6	CD096847	CD096847 ME1-0010T
	17	552.4	37.3	974	9	BZ440868	BZ440868 BONKT51TR
c	18	552.2	37.3	1106	9	BZ469058	BZ469058 BONHE54TF
c	19	551.6	37.3	1069	9	BZ474941	BZ474941 BONKR59TR
	20	543.8	36.8	725	7	CN204148	CN204148 Tor4539 G
c	21	543	36.7	899	9	BZ685785	BZ685785 PUBDT54TD
	22	542.4	36.7	977	9	BZ459292	BZ459292 BONKQ28TF
	23	542.2	36.7	762	8	DR385950	DR385950 RTHG1_11_
	24	536.8	36.3	951	9	BH651765	BH651765 BOMFE30TR
	25	527.4	35.7	1050	10	CW001852	CW001852 ZMMBHg000
	26	526.8	35.6	885	7	CN201712	CN201712 Tor1780 G
	27	523.8	35.4	947	9	BZ464837	BZ464837 BONKP76TR
c	28	522	35.3	1096	9	BZ502068	BZ502068 BONII25TR
	29	520.6	35.2	918	9	BZ437960	BZ437960 BONNV72TF
c	30	518.6	35.1	901	9	BZ461852	BZ461852 BONKO15TF
c	31	517.8	35.0	617	6	CD096968	CD096968 ME1-0011T
	32	516.4	34.9	915	7	CV287759	CV287759 aof01-13m
	33	515.6	34.9	875	7	CV292617	CV292617 aof01-2ms
	34	511.6	34.6	1082	9	BZ459110	BZ459110 BONBR59TR
	35	505.4	34.2	862	9	BH527452	BH527452 BOGVP36TR
	36	505	34.1	1030	9	BZ463792	BZ463792 BONKY05TR
	37	504.6	34.1	895	8	DR027023	DR027023 Osmo01058
c	38	504	34.1	889	9	BZ426275	BZ426275 BOOAB81TR
	39	502.8	34.0	1020	9	BH685417	BH685417 BOMFG90TR
	40	501.2	33.9	940	11	CT016030	CT016030 KBrH125K2
	41	501.2	33.9	955	11	CT013781	CT013781 KBrH122A0
	42	500.8	33.9	935	9	BZ468986	BZ468986 BONKD78TF
	43	500.8	33.9	950	7	CK285891	CK285891 EST748613
c	44	499.8	33.8	995	9	BH700021	BH700021 BOMND50TR
c	45	498.4	33.7	837	7	CV291378	CV291378 aof01-1ms

ALIGNMENTS

RESULT 1
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LOCUS BH771024 6499 bp DNA linear GSS 01-MAY-2002
DEFINITION LLMGtag746 MG1363 Random Sequence Tag Library Lactococcus lactis subsp. cremoris genomic, genomic survey sequence.
ACCESSION BH771024
VERSION BH771024.1 GI:20373981
KEYWORDS GSS.
SOURCE Lactococcus lactis subsp. cremoris
ORGANISM Lactococcus lactis subsp. cremoris
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
REFERENCE 1 (bases 1 to 6499)
AUTHORS Bolotin,A., Ehrlich,S.D. and Sorokin,A.
TITLE Studies of genomes of dairy bacteria Lactococcus lactis
JOURNAL Sci. Aliments (2002) In press
COMMENT Contact: Sorokin A
Genetique Microbienne
INRA
CRJ INRA, Domaine de Vilvert, 78352 Jouy en Josas cedex, France
Tel: 33 1 34 65 25 16
Fax: 33 1 34 65 25 21
Email: sorokine@jouy.inra.fr
best homologue in strain IL1403 is ywgA (78%)
Class: shotgun
High quality sequence start: 30
High quality sequence stop: 6471.
FEATURES Location/Qualifiers
source 1. .6499
/organism="Lactococcus lactis subsp. cremoris"
/mol_type="genomic DNA"
/strain="MG1363"
/sub_species="cremoris"
/db_xref="taxon:1359"
/clone_lib="MG1363 Random Sequence Tag Library"
/note="Vector: pSGMU2; Site_1: SmaI; Library of chromosomal fragments of L.lactis strain MG1363 was prepared by partial AluI digestion or by sonication."
ORIGIN

Query Match 55.2%; Score 817; DB 9; Length 6499;
Best Local Similarity 75.6%; Pred. No. 3.6e-215;
Matches 1147; Conservative 0; Mismatches 325; Indels 45; Gaps 9;

Qy 1 AGAGTTTGATCCTGGCTCAGGACGAACGCTGGCGGCGTGCTTAACACATGCAAGTCGAGC 60

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:12:04 ; Search time 1667 Seconds
(without alignments)
5913.066 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_21:*
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3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*
14: geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1330.6	90.0	1440	14	ADZ35975	Adz35975 Verrucosi
2	1283.6	86.8	1403	12	ADJ38609	Adj38609 Micromono
3	1261.6	85.3	1514	14	ADW12667	Adw12667 Rhodococc
4	1255.2	84.9	1511	13	ADR90325	Adr90325 Rhodococc
5	1251.4	84.6	1488	13	ADS17269	Ads17269 Lechevali
6	1250.4	84.5	1471	12	ADF56671	Adf56671 YS-45494
7	1250.4	84.5	1471	12	ADG64520	Adg64520 Saccharot
8	1250.4	84.5	1471	14	ADY86148	Ady86148 Saccharot
9	1235.2	83.5	1480	3	AAA40374	Aaa40374 Rhodococc
10	1235.2	83.5	1480	3	AAA40373	Aaa40373 Rhodococc
11	1235	83.5	1517	12	ADM92517	Adm92517 Gordonia
12	1235	83.5	1517	12	ADO71823	Ado71823 DNA of RN
13	1229.6	83.1	1511	13	ADR90327	Adr90327 Rhodococc
14	1228.4	83.1	1437	12	ADF56670	Adf56670 YS-44442
15	1228.4	83.1	1437	12	ADG64519	Adg64519 Saccharot
16	1228.4	83.1	1437	14	ADY86147	Ady86147 Saccharot
17	1223.8	82.7	1482	14	AEA22404	Aea22404 Mycobacte
18	1220	82.5	1455	14	AEA22412	Aea22412 Mycobacte
19	1219	82.4	1492	14	ADZ69170	Adz69170 Marine ac
20	1217.4	82.3	1492	14	ADZ69171	Adz69171 Marine ac
21	1213.6	82.1	1514	13	ADR90326	Adr90326 Rhodococc
22	1211	81.9	1492	14	ADZ69172	Adz69172 Marine ac
23	1208.2	81.7	1457	6	ABN86275	Abn86275 G. polyis
24	1206.2	81.6	1457	6	ABN86276	Abn86276 G. polyis
25	1194.8	80.8	1449	14	AEA22405	Aea22405 Mycobacte
26	1192	80.6	1474	14	ADZ69169	Adz69169 Marine ac
27	1188.8	80.4	1524	11	AEB80307	Aeb80307 Organic w
28	1185	80.1	1525	11	AEB80304	Aeb80304 Organic w
29	1183.8	80.0	1484	14	AEA22414	Aea22414 Mycobacte
30	1180	79.8	1452	2	AAX82004	Aax82004 Curtobact
31	1177.2	79.6	1443	14	ADX38843	Adx38843 Microbisp
32	1175.6	79.5	1517	11	AEB80305	Aeb80305 Organic w
33	1172	79.2	1449	2	AAQ37639	Aaq37639 Mycobacte
c 34	1168.2	79.0	2743	4	AAS59540	Aas59540 Propionib
c 35	1168.2	79.0	2743	8	ACF64469	Acf64469 Propionib
36	1166.8	78.9	1439	14	AEA22403	Aea22403 Mycobacte
37	1166.8	78.9	1524	4	AAS30719	Aas30719 Mycobacte
38	1166.8	78.9	1536	10	ADB61681	Adb61681 16S rRNA
39	1166.8	78.9	1536	10	ADB61682	Adb61682 16S rRNA
40	1166.8	78.9	1537	10	ADF41649	Adf41649 Mycobacte
41	1166.8	78.9	110000	4	AAI99682_14	Continuation (15 o
42	1166.8	78.9	110000	4	AAI99683_14	Continuation (15 o
43	1161.6	78.5	1508	14	ADZ69174	Adz69174 Marine ac
44	1161.4	78.5	1503	14	ADZ69173	Adz69173 Marine ac
45	1153.6	78.0	1461	14	AEA22406	Aea22406 Mycobacte

ALIGNMENTS

RESULT 1
ADZ35975
ID ADZ35975 standard; DNA; 1440 BP.
XX
AC ADZ35975;
XX
DT 30-JUN-2005 (first entry)
XX
DE Verrucosispora sp. AB-18-032 16S rRNA gene.
XX
KW ds; antibiotic; antimalarial; protozoacide; 16S rRNA;
KW polycyclic macrolactone; abyssomicin; p-Aminobenzoic acid; folic acid;
KW vitamin; abyssomicin B; abyssomicin C; abyssomicin D;
KW Staphylococcus aureus infection; protozoal infection;
KW plasmodium infection; Leishmania infection; chagas disease;
KW Gram positive bacteria infection; mrsa infection .
XX
OS Verrucosispora sp. AB-18-032.
XX
PN WO2005033114-A1.
XX
PD 14-APR-2005.
XX
PF 23-SEP-2004; 2004WO-EP010661.
XX
PR 01-OCT-2003; 2003DE-01047472.
PR 11-NOV-2003; 2003DE-01053300.
XX
PA (UYTU-) UNIV TUEBINGEN.
XX
PI Fiedler H, Suessmuth R, Zaehner H, Bull A;
XX
DR WPI; 2005-296122/30.
XX
PT New abyssomicin polycyclic macrolactone compounds, useful as antibiotics
PT and antiprotozoal agents effective against multiresistant strains,
PT prepared using bacteria of genus Verrucosispora.
XX
PS Disclosure; SEQ ID NO 1; 47pp; German.
XX
CC This invention describes novel polycyclic macrolactones and their
CC derivatives , prepared using bacteria of genus Verrucosispora and

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:09:44 ; Search time 7424 Seconds
(without alignments)
11324.281 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
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9: gb_ro:*
10: gb_sts:*
11: gb_sy:*
12: gb_un:*
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14: gb_htg:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1479	100.0	1479	1	AY040619	AY040619 Salinospo
	2	1479	100.0	1479	1	AY040620	AY040620 Salinospo
	3	1479	100.0	1479	1	AY040621	AY040621 Salinospo
	4	1479	100.0	1479	1	AY464534	AY464534 Salinospo
	5	1478	99.9	1479	1	AY464533	AY464533 Salinospo
	6	1478	99.9	1479	1	AY562205	AY562205 Salinospo
	7	1477.4	99.9	1479	1	AY040623	AY040623 Salinospo
	8	1476.4	99.8	1479	1	AY562198	AY562198 Salinospo
	9	1476.4	99.8	1479	1	AY562204	AY562204 Salinospo
	10	1476.4	99.8	1479	1	AY562206	AY562206 Salinospo
	11	1474.8	99.7	1479	1	AY562201	AY562201 Salinospo
	12	1473.2	99.6	1479	1	AY562202	AY562202 Salinospo
	13	1468.4	99.3	1479	1	AY562199	AY562199 Salinospo
	14	1467.8	99.2	1479	1	AY040618	AY040618 Salinospo
	15	1467.8	99.2	1479	1	AY040622	AY040622 Salinospo
	16	1467.8	99.2	1480	1	AY040617	AY040617 Salinispo
	17	1464.6	99.0	1480	1	AY464535	AY464535 Salinospo
	18	1462	98.9	1479	1	AY562197	AY562197 Salinospo
	19	1459	98.6	1480	1	AY562200	AY562200 Salinospo
	20	1454	98.3	1479	1	AY562203	AY562203 Salinospo
	21	1429	96.6	1479	1	AY878316	AY878316 Salinospo
c	22	1414.2	95.6	38146	1	AY524043	AY524043 Micromono
	23	1409.4	95.3	1479	1	AY040625	AY040625 Micromono
	24	1405.8	95.1	1507	1	AB193564	AB193564 Micromono
	25	1405.8	95.1	1508	1	AB193563	AB193563 Micromono
	26	1404.8	95.0	1508	1	AB193562	AB193562 Micromono
	27	1403.6	94.9	1482	1	AB159779	AB159779 Micromono
	28	1403	94.9	1470	1	MMRRN16S	X92596 M.melanospo
	29	1402.4	94.8	1476	1	MGL16SRRN	X92615 M.globosa 1
	30	1401.8	94.8	1476	1	MCI16SRRN	X92617 M.citrea 16
	31	1401.4	94.8	1479	1	AY040624	AY040624 Micromono
	32	1400.8	94.7	1471	1	MEP16SRRN	X92608 M.echinospo
	33	1400.2	94.7	1474	1	MEA16SRRN	X92618 M.echinoaur
	34	1400.2	94.7	1476	1	MPRRN16S	X92595 M.purpurea
	35	1399.8	94.6	1480	1	AY534920	AY534920 Actinomyc
	36	1399.4	94.6	1477	1	MEN560635	AJ560635 Micromono
	37	1399	94.6	1466	1	MERRN16S	X92597 M.echinospo
	38	1399	94.6	1466	1	MR16RRNA	X92612 M.rhodorang
	39	1398.6	94.6	1477	1	MAU245712	AJ245712 Micromono
	40	1398.6	94.6	1477	1	MRO16SRRN	X92631 M.rosaria 1
	41	1396.6	94.4	1509	1	AJ783989	AJ783989 Micromono
	42	1396.6	94.4	1509	1	AJ783992	AJ783992 Micromono
	43	1396.6	94.4	1510	1	AJ783994	AJ783994 Micromono
	44	1396	94.4	1472	1	MEB16SRRN	X92625 M.echinobru
	45	1395.4	94.3	1476	1	MN16RRNA	X92602 M.narashino

ALIGNMENTS

RESULT 1
AY040619
LOCUS AY040619 1479 bp DNA linear BCT 08-JUN-2005
DEFINITION Salinospora sp. CNH643 16S ribosomal RNA gene, partial sequence.
ACCESSION AY040619
VERSION AY040619.2 GI:67043491
KEYWORDS .
SOURCE Salinispora arenicola
ORGANISM Salinispora arenicola
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micromonosporineae; Micromonosporaceae; Salinispora.
REFERENCE 1 (bases 1 to 1479)
AUTHORS Mincer,T.J., Jensen,P.R., Kauffman,C.A. and Fenical,W.
TITLE Widespread and persistent populations of a major new marine actinomycete taxon in ocean sediments
JOURNAL Appl. Environ. Microbiol. 68 (10), 5005-5011 (2002)
PUBMED 12324350
REFERENCE 2 (bases 1 to 1479)
AUTHORS Mincer,T.J., Jensen,P.R., Kauffman,C.A. and Fenical,W.H.
TITLE Direct Submission
JOURNAL Submitted (15-JUN-2001) Marine Chemistry, Scripps Institution of Oceanography, UCSD, 8602 La Jolla Shores Dr., La Jolla, CA 92093-0204, USA
REFERENCE 3 (bases 1 to 1479)
AUTHORS Jensen,P.R., Mincer,T.J. and Fenical,W.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2005) CMBB, Scripps Institution of Oceanography, Mail Code 0204, La Jolla, CA 92093, USA
REMARK Sequence update by submitter
COMMENT On Jun 8, 2005 this sequence version replaced gi:22474396.
FEATURES Location/Qualifiers
source 1. .1479
/organism="Salinispora arenicola"
/mol_type="genomic DNA"
/strain="CNH643"
/db_xref="taxon:168697"
rRNA <1. .>1479
/product="16S ribosomal RNA"
ORIGIN

Query Match 100.0%; Score 1479; DB 1; Length 1479;

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 16, 2006, 00:04:50 ; Search time 788 Seconds
(without alignments)
7559.850 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9281099 seqs, 2013915447 residues

Total number of hits satisfying chosen parameters: 18562198

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_New:*
1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US06_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US09_NEW_PUB.seq1:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq1:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq2:*
10: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq3:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq2:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq3:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq4:*
15: /SIDS5/ptodata/2/pubpna/US60_NEW_PUB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:35:29 ; Search time 524 Seconds
(without alignments)
8702.075 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 6753657 seqs, 1541544009 residues

Total number of hits satisfying chosen parameters: 13507314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_New:*
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2: /SIDS5/ptodata/2/pna/US06_NEW_COMB.seq:*
3: /SIDS5/ptodata/2/pna/US07_NEW_COMB.seq:*
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5: /SIDS5/ptodata/2/pna/US09_NEW_COMB.seq:*
6: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq:*
7: /SIDS5/ptodata/2/pna/US10_NEW_COMB.seq1:*
8: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq:*
9: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq1:*
10: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq2:*
11: /SIDS5/ptodata/2/pna/US11_NEW_COMB.seq3:*
12: /SIDS5/ptodata/2/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1183.6	80.0	1487	8	US-11-335-686-1	Sequence 1, Appli
	2	1177.2	79.6	1443	7	US-10-521-336-1	Sequence 1, Appli
	3	869.6	58.8	2944528	10	US-11-045-004-1	Sequence 1, Appli
c	4	869.6	58.8	2944528	10	US-11-045-004-1	Sequence 1, Appli
	5	868.2	58.7	1555	5	US-09-941-095-160	Sequence 160, App
	6	865.4	58.5	1554	11	US-11-348-413-10825	Sequence 10825, A
	7	863.6	58.4	1504	10	US-11-273-617-10	Sequence 10, Appl
	8	858	58.0	1587	10	US-11-273-617-8	Sequence 8, Appli
	9	851.8	57.6	1538	11	US-11-348-413-12	Sequence 12, Appl
	10	851.8	57.6	1541	8	US-11-370-472-18	Sequence 18, Appl
	11	850.2	57.5	1513	8	US-11-370-472-10	Sequence 10, Appl
	12	845.8	57.2	1540	8	US-11-370-472-30	Sequence 30, Appl
	13	845.4	57.2	1541	8	US-11-370-472-19	Sequence 19, Appl
	14	843.8	57.1	1550	8	US-11-370-472-64	Sequence 64, Appl
	15	843.8	57.1	1550	8	US-11-370-472-65	Sequence 65, Appl
	16	843.8	57.1	1550	8	US-11-370-472-66	Sequence 66, Appl
	17	843.8	57.1	1550	8	US-11-370-472-67	Sequence 67, Appl
	18	843.8	57.1	1550	8	US-11-370-472-68	Sequence 68, Appl
	19	843.8	57.1	1550	8	US-11-370-472-69	Sequence 69, Appl
	20	843.8	57.1	2160266	7	US-10-513-024-1373	Sequence 1373, Ap
	21	843.2	57.0	1568	10	US-11-273-617-1	Sequence 1, Appli

GenCore version 5.1.7

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 22:19:09 ; Search time 8961 Seconds
(without alignments)
9125.795 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 79147668 seqs, 27645789525 residues

Total number of hits satisfying chosen parameters: 158295336

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_NA_Main:*
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3: /cgn2_6/ptodata/1/pna/PCTUSC_COMB.seq:*
4: /cgn2_6/ptodata/1/pna/US06_COMB.seq:*
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10: /cgn2_6/ptodata/1/pna/US080_COMB.seq:*
11: /cgn2_6/ptodata/1/pna/US081_COMB.seq:*
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16: /cgn2_6/ptodata/1/pna/US086_COMB.seq:*
17: /cgn2_6/ptodata/1/pna/US087_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2006, 23:49:41 ; Search time 1329 Seconds
(without alignments)
9202.716 Million cell updates/sec

Title: US-09-991-518C-4
Perfect score: 1479
Sequence: 1 agagtttgatcctggctcag.....agtcgtaacaaggtagccgt 1479

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA_Main:*
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES